

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: MAERTENS, GEERT; STUYVER, LIEVEN;
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO

(ii) TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
ISOLATES

(iii) NUMBER OF SEQUENCES: 97

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: BIERMAN & MUSERLIAN
(B) STREET: 600 THIRD AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10016

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/256,568
(B) FILING DATE: 18-JUL-1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/EP93/03325
(B) FILING DATE: 26-NOV-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP/93/402,129.6
(B) FILING DATE: 31-AUG-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP/92/403,222.0
(B) FILING DATE: 27-NOV-1992

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 19,683
(C) REFERENCE/DOCKET NUMBER: 410.004

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 661-8000
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05669303-070604

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV

(B) MAP POSITION: Position -299 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..27

(D) OTHER INFORMATION: /standard_name=
"Universal HCV primer HcPr98"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCCTGTGAGG AACTWCTGTC TTCACGC

27

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV (Okamoto et al.,
1991)

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- (viii) POSITION IN GENOME:
 (A) CHROMOSOME/SEGMENT: HCV
 (B) MAP POSITION: Position -1 of 5' end

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..21
 (D) OTHER INFORMATION: /standard_name=
 "Universal HCV primer HcPr29"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGTGCACGGT CTACGAGACC T

21

- (2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: genomic DNA

- (iii) HYPOTHETICAL: YES

- (iii) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: HCV

- (viii) POSITION IN GENOME:
 (A) CHROMOSOME/SEGMENT: HCV
 (B) MAP POSITION: Position -264 of 5' end

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..26
 (D) OTHER INFORMATION: /standard_name=
 "Universal HCV primer HcPr95"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TCTAGCCATG GCGTTAGTRY GAGTGT

26

- (2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV

(B) MAP POSITION: Position -29 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..26

(D) OTHER INFORMATION: /standard_name=
"Universal HCV primer HcPr96"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CACTCGCAAG CACCCTATCA GGCAGT

26

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 1 (Kato et al.,
1990)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 1

(B) MAP POSITION: position -170 of the 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

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- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 1 specific Probe HcPr124"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AATTGCCAGG ACGACC

16

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: YES
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HCV type 1 (Kato et al., 1990)
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: HCV type 1
 - (B) MAP POSITION: position -117 of 5'end
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..16
 - (D) OTHER INFORMATION: /standard_name= "HCV type 1 specific Probe HcPr125"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TCTCCAGGCA TTGAGC

16

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA

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(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 1b (Kato et al., 1990)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 1b

(B) MAP POSITION: position -103 of the 5'end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type 1b specific Probe HcPr138"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CCGCGAGACT GCTAGC

16

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 2

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 2

(B) MAP POSITION: position -83 of the 5'end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type 2 specific Probe HcPr147"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TAGCGTTGGG TTGCGA

16

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HCV type 2a (Chan et al., 1992)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: HCV type 2a
- (B) MAP POSITION: position -168 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 2a specific probe HcPr136"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTRCCGGRAA GACTGG

16

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

1990/07/06 07:06:01

(C) INDIVIDUAL ISOLATE: HCV type 2a (Chan et al., 1992)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: HCV type 2a
- (B) MAP POSITION: Position -117 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 2a specific probe HcPr137"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TGRCCGGGCA TAGAGT

16

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HCV type 2b (Nakao et al., 1991)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: HCV type 2b
- (B) MAP POSITION: position -168 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 2b specific probe HcPr126"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TTACCGGGAA GACTGG

16

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(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: YES
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HCV type 2b (Nakao et al., 1991)
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: HCV type 2b
 - (B) MAP POSITION: position -117 of 5' end
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..16
 - (D) OTHER INFORMATION: /standard_name= "HCV type 2b specific probe HcPr127"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TGACCGGACA TAGAGT

16

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HCV type 3
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: HCV type 3
 - (B) MAP POSITION: position -170 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 3 specific probe HcPr128"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

AATCGCTGGG GTGACC

16

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HCV type 3

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: HCV type 3
- (B) MAP POSITION: position -117 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 3 specific probe HcPr 129"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TTTCTGGGTA TTGAGC

16

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TCTTGGAACA ACCCGC

16

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HCV type 4 (Bukh et al., 1992)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: HCV type 4
- (B) MAP POSITION: position -170 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 4 specific probe HcPr 144"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AATYGCCGGG ATGACC

16

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 4

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 4

(B) MAP POSITION: position -147 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type
4 specific probe HcPr145"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TTCTTGGAAC TAACCC

16

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 4

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 4

(B) MAP POSITION: position -117 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type
4 specific probe HcPr146"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TTTCCGGGCA TTGAGC

16

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(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HCV (Kato et al., 1990)
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: HCV
 - (B) MAP POSITION: position -115 of 5' end
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..16
 - (D) OTHER INFORMATION: /standard_name="Universal HCV probe HcPr 142"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTGGGCGYGC CCCCCG

16

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HCV type 3
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: HCV type 3
 - (B) MAP POSITION: position -103 of 5' end

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 3 specific probe HcPr 154"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CCGCGAGATC ACTAGC

16

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HCV type 2a (Okamoto et al., 1991)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: HCV type 2a
- (B) MAP POSITION: position -165 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 2a specific probe HcPr156"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CCGGGAAGAC TGGGTC

16

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

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(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 2b (Okamoto et al., 1992)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 2b

(B) MAP POSITION: position - 165 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type 2b specific probe HcPr157"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CCGGAAAGAC TGGGTC

16

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 2a (Okamoto et al., 1991)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 2a

(B) MAP POSITION: position -136 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type 2a specific probe HcPr158"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

ACCCACTCTA TGCCCCG

16

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HCV type 2b (Okamoto et al., 1992)

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: HCV type 2b
- (B) MAP POSITION: position -136 of 5' end

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /standard_name= "HCV type 2b specific probe HcPr159"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ACCCACTCTA TGTCCG

16

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

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(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV type 2 (Okamoto et al., 1992)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV type 2

(B) MAP POSITION: position -126 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "HCV type 2 specific probe HcPr160"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

ATAGAGTGGG TTTATC

16

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HCV (Kato et al., 1990)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: HCV

(B) MAP POSITION: Position -195 of 5' end

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /standard_name= "Universal HCV probe HcPr153"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TCTGCGGAAC CGGTGA

16

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(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

AATTGCCAGG AYGACC

16

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GCTCAGTGCC TGGAGA

16

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: NO

09899302-070601

CCGCGAGACY GCTAGC

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CCCCGCAAGA CTGCTA

16

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CGTACAGCCT CCAGGC

16

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

16

16

16

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

CCGCAAGATC ACTAGC

16

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GAGTGTTGTA CAGCCT

16

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

AATCGCCGGG ATGACC

16

066530-07601
1999/02/20 09:30

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GAGTGTTGTG CAGCCT

16

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

AATCGCCGGG ACGACC

16

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

09699302.070604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

AATGCCCGGC AATTTG

16

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

AATCGCCGAG ATGACC

16

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AATGCTCGGA AATTTG

16

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

1990/02/20 09:00

(iii) ANTI-SENSE: NO

GAGTGTCGAA CAGCCT

16

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

AATTGCCGGG ATGACC

16

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

TCTCCGGGCA TTGAGC

16

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

AATTGCCGGG ACGACC

16

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

GGGTCCTTTC CATTGG

16

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

AATCGCCAGG ATGACC

16

0969302-070601

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

16

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

16

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

AGTYCACCGG AATCGC

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGAATCGCCA GGACGA

16

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GAATCGCCGG GTTGAC

16

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(B) CLONE: j p 62

(B) MAP POSITION: 5' untranslated region

GAGTGTCTGTA	CAGCCTCCAG	GCCCCCCCCT	CCCGGGAGAG	40
CCATAGTGGT	CTGCGGAACC	GGTGAGTACA	CCGGAATTGC	80
CGGGAAGACT	GGGTCCTTTC	TTGGATAAAC	CCACTCTATG	120
CCCGGCCATT	TGGGCGTGCC	CCCGCAAGAC	TGCTAGCCGA	160
GTAGCGTTGG	GTTGCGA			177

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb81

(B) MAP POSITION: 5' untranslated region

GAGTGTCTGTA	CAGCCTCCAG	GCCCCCCCCT	CCCGGGAGAG	40
CCATAGTGGT	CTGCGGAACC	GGTGAGTACA	CCGGAATCGC	80
CGGGAAGACT	GGGTCCTTTC	TTGGATAAAC	CCACTCTATG	120
CCCGGTCATT	TGGGCGTGCC	CCCGCAAGAC	CGCTAGCCGA	160
GTAGCGTTGG	GTTGCGA			177

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: br56

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GAGTGTCTGTG CAGCCTCCAG GCCCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA	120
CCCAGAAATT TGGGCGTGCC CCCGCGAGAT CACTAGCCGA	160
GTAGTGTTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: bu79

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5'untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GAGTGTTGTA CAGCCTCCAG GCCCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGACGACC GGGTCCTTTC TTGGATTAAAC CCGCTCAATG	120
CCCGGAAATT TGGGCGTGCC CCCGCGAGAC TGCTAGCCGA	160
GTAGTGTTGG GTCGCGA	177

09866303-070601

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: bu74

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GAGTGTGTG CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTCCA CCGGAATCGC	80
CGGGATGACC GGGTCCTTTC TTGGAATAA CCCGCTCAAT	120
GCCCGGAAAT TTGGGCGTGC CCCGCGAGA CTGCTAGCCG	160
AGTAGTGTG GGTGCGCA	178

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb80

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GAGTGTCGTG CAGCCTCCAG GCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGATGACC GGGTCCTTTC TTGGAATAA CCCGCTCAAT	120

099070-2066880

GCCCGGAAAT TTGGGCGTGC CCCCGCGAGA CTGCTAGCCG 160
AGTAGTGTTG GGTCCGCA 178

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: be82 (also referred to as be99)

- (viii) POSITION IN GENOME:
 (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GAGTGTCGTG CAGCCTCCAG GACCCCCCT CCCGGGAGAG 40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGAATTGC 80
CAGGACGACC GGGTCCTTTC TTGGATCAAC CCGCTCAATG 120
CCTGGAGATT TGGGCGTGCC CCCGCGAGAC CGCTAGCCGA 160
GTAGTGTTGG GTCGCA 177

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: be90

- (viii) POSITION IN GENOME:
 (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GAGTGTCGTG CAGCCTCCAG GATCCCCCT CCCGGGAGAG 40

09899302-070604

(2) INFORMATION FOR SEQ ID NO: 63:

- | | | | | |
|-------------|------------|------------|------------|-----|
| GAGTGTCTGTA | CAGCCTCCAG | GCCCCCCCCT | CCCGGGAGAG | 40 |
| CCATAGTGGT | CTGCGGAACC | GGTGAGTACA | CCGGAATTGC | 80 |
| CGGAAAGACT | GGGTCCTTTC | TTGGATAAAC | CCACTCTATG | 120 |
| TCCGGTCATT | TGGGCGTGCC | CCCGCAAGAC | TGCTAGCCTA | 160 |
| GTAGCGTTGG | GTTGCGA | | | 177 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
(vii) IMMEDIATE SOURCE:
(B) CLONE: be92

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GAGTGTCTGTA CAGCCTCCAG GGGGGGGGCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	80
CAGGAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG	120
CCTGGTCATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGCGTTGG GTTGCGA	177

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: be93

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GAGTGTCTGTG CAGCCTCCAG GGGGGGGGCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA	120
CCCAGACATT TGGGCGTGCC CCCGCGAGAT CACTAGCCGA	160
GTAGTGTTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

09869302-070601

- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: be94
- (viii) POSITION IN GENOME:
 - (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GAGTGTCGTG CAGCCTCCAG GGGGGGGGCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA	120
CCCAGACATT TGGGCGTGCC CCCGCAAGAT CACTAGCCGA	160
GTAGTGTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: gb48
- (viii) POSITION IN GENOME:
 - (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GAGTGTGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGGGATGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG	120
CCCGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTGG GTCGCGA	177

095930-070501

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: gb116

(viii) POSITION IN GENOME:
 (B) MAP POSITION: 5' untranslated region

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

GAGTGTTGTA CAGCCTCCAG GACCCCCCCT CCCGGGAGAG          40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC          80
CGGGATGACC GGGTCCTTTC TTGGATTAAAC CCGCTCAATG        120
CCCGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA        160
GTAGTGTTGG GTCGCGA                                177

```

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: gb569

(viii) POSITION IN GENOME:
 (B) MAP POSITION: 5' untranslated region

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      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:
GAGTGTTGTA CAGCCTCCAG GACCCCCCCT CCCGGGAGAG          40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC          80
CGGGATGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG         120

```

CCCGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA 160
GTAGTGTGG GTCGCGA 177

(2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: gb358

- (viii) POSITION IN GENOME:
 - (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GAGTGTGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG 40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC 80
CGGGATGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG 120
CCCGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA 160
GTAGTGTGG GTCGCGA 177

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: gb549

- (viii) POSITION IN GENOME:
 - (B) MAP POSITION: 5' untranslated region

099303-070604

GAGTGTGTG	CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	40
CCATAGTGGT	CTGCGGAACC	GGTGAGTTCA	CCGGAATCGC	80
CGGGACGACC	GGGTCCTTTC	TTGGAACAAA	CCCGCTCAAT	120
GCCCGGCAAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	160
AGTAGTGTTG	GGTCGCGA			178

(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: cam600

(B) MAP POSITION: 5' untranslated region

GAGTGT	TGTA	CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	40
CCATAG	TGGT	CTGCGGAACC	GGTGAGTACA	CCGGAATCGC	80
CGAGAT	GACC	GGGTCCTTTC	TTGGATCAAC	CCGCTCAATG	120
CTCGGA	AATT	TGGGCGTGCC	CCCGCAAGAC	TGCTAGCCGA	160
GTAGTG	TTGG	GTCGCGA			177

(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: cam736

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

GAGTGTGTGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGAGATGACC GGGTCCTTTC TTGGATCAAC CCGCTCAATG	120
CTCGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: gb809

(viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

GAGTGTGTGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CGAGATGACC GGGTCCTTTC TTGGATCAAC CCGCTCAATG	120
CTCGGAAATT TGGGCGTGCC CCCGCAAGAC CGCTAGCCGA	160
GTAGTGTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid

109070-20265860

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb487

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GAGTGTGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CAGGATGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG	120
CCTGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTGTTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb724

(viii) POSITION IN GENOME:

(B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

GAGTGTCGTA CAGCCTCCAG GACCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTTCA CCGGAATCGC	80
CAGGACGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG	120
CCTGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTGTTGG GTCGCGA	177

0699362-070601

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: be97

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GAGTGTTGTA CAGCCTCCAG GACCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	80
CAGGACGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG	120
CCTGGAAATT TGGGCGTGCC CCCGCAAGAC TGCTAGCCGA	160
GTAGTGTTGG GTCGCGA	177

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: be95

(viii) POSITION IN GENOME:

- (B) MAP POSITION: 5' untranslated region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

GAGTGTCGAA CAGCCTCCAG GACCCCCCCT CCCGGGAGAG	40
CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	80
CGGGATGACC GGGTCCTTTC TTGGATTAAC CCGCTCAATG	120

(2) INFORMATION FOR SEQ ID NO: 79:

- (ii) MOLECULE TYPE: cDNA

- (viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

- | | | | | |
|-------------|------------|------------|------------|-----|
| GAGTGTCTGAA | CAGCCTCCAG | GACCCCCCCT | CCCGGGAGAG | 40 |
| CCATAGTGGT | CTGCGGAACC | GGTGAGTACA | CCGGAATTGC | 80 |
| CGGGACGACC | GGGTCCTTTC | TTGGATAAAC | CCGCTCAATG | 120 |
| CCCGGAGATT | TGGGCGTGCC | CCCGCGAGAC | TGCTAGCCGA | 160 |
| GTAGTGTTGG | GTCGCGA | | | 177 |

(2) INFORMATION FOR SEQ ID NO: 80:

- (ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
(B) CLONE: be98

- (viii) POSITION IN GENOME:
(B) MAP POSITION: 5' untranslated region

GAGTGTCTGTG	CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	40
CCATAGTGGT	CTGCGGAACC	GGTGAGTACA	CCGGAATCGC	80
CGGGTTGACC	GGGTCCTTTC	TTGGAACTAC	CCGCTCAATG	120
CCCGGAAATT	TGGGCGTGCC	CCGCGAGAC	TGCTAGCCGA	160
GTAGTGTGTTGG	GTCGCGA			177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: gb438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

GAGTGTCTGAA	CAGCCTCCAG	GATCCCCCCT	CCCGGGAGAG	40
CCATAGTGGT	CTGCGGAACC	GGTGAGTTCA	CCGGAATCGC	80
CGGGATGACC	GGGTCCTTTC	TTGGAATCAA	CCCGCTCAAT	120
GCCCGGAAAT	TTGGGCGTGC	CCCCGCGAGA	CTGCTAGCCG	160
AGTAGTGTTG	GGTCGCGA			178

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: be90

(viii) POSITION IN GENOME:

(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu
1          5          10
Ser Ile Tyr Gln Cys Cys Asp Leu Ala Pro Glu Ala
          15          20
Arg Gln Ala Ile Lys Ser Leu Thr Glu Arg Leu Tyr
25          30          35
Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
          40          45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu
50          55          60
Thr Thr Ser Cys Gly Asn Thr Leu Thr Cys Tyr Leu
          65          70
Lys Ala Ser Ala Ala Cys Arg Ala Ala Lys Leu Gln
          75          80
Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85          90          95
Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala
          100         105
Ala Ser Leu Arg Val
          110

```

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: be91

(viii) POSITION IN GENOME:

(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu
1          5          10
Ser Ile Tyr Gln Ala Cys Ser Leu Pro Gln Glu Ala
          15          20

```

(2) INFORMATION FOR SEO ID NO: 84:

(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Thr	Glu	Glu
1				5					10		
Ser	Ile	Tyr	Leu	Ala	Cys	Ser	Leu	Pro	Glu	Gln	Ala
		15					20				
Arg	Thr	Ala	Ile	His	Ser	Leu	Thr	Glu	Arg	Leu	Tyr
25				30						35	
Val	Gly	Gly	Pro	Met	Leu	Asn	Ser	Lys	Gly	Gln	Thr
			40					45			
Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Phe
	50					55					60
Thr	Thr	Ser	Met	Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Val
				65					70		
Lys	Ala	Gln	Ala	Ala	Cys	Lys	Ala	Ala	Gly	Ile	Ile
		75					80				
Ala	Pro	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val
85				90						95	

Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu
 100 105
 Arg Asn Leu Arg Ala
 110

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: be93

(viii) POSITION IN GENOME:

(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu
 1 5 10
 Glu Ile Tyr Gln Cys Cys Asn Leu Glu Pro Glu Ala
 15 20
 Arg Lys Val Ile Ser Ser Leu Thr Glu Arg Leu Tyr
 25 30 35
 Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Ala Gln
 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu
 50 55 60
 Pro Thr Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile
 65 70
 Lys Ala Thr Thr Ala Ala Lys Ala Ala Gly Leu Arg
 75 80
 Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg
 100 105
 Ala Ala Leu Arg Ala
 110

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

0989302-070601

- (ii) MOLECULE TYPE: protein
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: gb48
- (viii) POSITION IN GENOME:
 - (B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu
1          5          10
Glu Val Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala
15          20
Arg Lys Ala Ile Thr Ala Leu Thr Glu Arg Leu Tyr
25          30          35
Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
40          45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr
50          55          60
Thr Thr Ser Phe Gly Asn Thr Leu Thr Cys Tyr Leu
65          70
Lys Ala Ser Ala Ala Ile Lys Ala Ala Gly Leu Arg
75          80
Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85          90          95
Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys
100          105
Arg Pro Leu Gly Ala
110

```

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: gb116
- (viii) POSITION IN GENOME:
 - (B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

```

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu
1          5          10

```

L09070-295660

Glu Val Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala
 15 20
 Arg Arg Ala Ile Thr Ala Leu Thr Glu Arg Leu Tyr
 25 30 35
 Val Gly Gly Pro Met His Asn Ser Arg Gly Asp Leu
 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr
 50 55 60
 Thr Thr Ser Phe Gly Asn Thr Leu Thr Cys Tyr Leu
 65 70
 Lys Ala Ser Ala Ala Ile Arg Ala Ala Gly Leu Arg
 75 80
 Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys
 100 105
 Arg Ala Leu Gly Ala
 110

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: gb215

(viii) POSITION IN GENOME:

- (B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu
 1 5 10
 Glu Val Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala
 15 20
 Arg Lys Val Ile Thr Ala Leu Thr Glu Arg Leu Tyr
 25 30 35
 Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr
 50 55 60
 Thr Thr Ser Phe Gly Asn Thr Leu Thr Cys Tyr Leu
 65 70
 Lys Ala Ser Ala Ala Ile Arg Ala Ser Gly Leu Arg
 75 80

009020 20E66650

(2). INFORMATION FOR SEQ ID NO: 89:

(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

(2) INFORMATION FOR SEQ ID NO: 90:

(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: gb549

(viii) POSITION IN GENOME:

(B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu
1 5 10
Glu Ile Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala
15 20
Arg Lys Val Ile Ser Ala Leu Thr Glu Arg Leu Tyr
25 30 35
Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu
40 45
Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr
50 55 60
Thr Thr Ser Phe Gly Asn Thr Val Thr Cys Tyr Leu
65 70
Lys Ala Val Ala Ala Thr Arg Ala Ala Gly Leu Lys
75 80
Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala
100 105
Arg Ala Leu Arg Ala
110

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: gb809

0969366-070601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```

Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu
1          5          10
Glu Val Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala
          15          20
Arg Lys Val Ile Ala Ala Leu Thr Glu Arg Leu Tyr
25          30          35
Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
          40          45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr
50          55          60
Thr Thr Ser Phe Gly Asn Thr Met Thr Cys Tyr Leu
          65          70
Lys Ala Ser Ala Ala Ile Arg Ala Ala Gly Leu Lys
          75          80
Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85          90          95
Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys
          100          105
Arg Ala Leu Gly Ala
          110

```

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: be95

(viii) POSITION IN GENOME:

- (B) MAP POSITION: ns5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu
1          5          10
Ser Ile Tyr Gln Ser Cys Asp Leu Gln Pro Glu Ala
          15          20
Arg Ala Ala Ile Arg Ser Leu Thr Gln Arg Leu Tyr
25          30          35
Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln
          40          45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe
50          55          60

```

0969302.070601

Thr	Thr	Ser	Met	Gly	Asn	Thr	Met	Thr	Cys	Tyr	Ile
				65					70		
Lys	Ala	Leu	Ala	Ser	Cys	Arg	Ala	Ala	Arg	Leu	Arg
		75					80				
Asp	Cys	Thr	Leu	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val
85					90					95	
Ala	Ile	Cys	Glu	Ser	Gln	Gly	Thr	His	Glu	Asp	Glu
			100					105			
Ala	Ser	Leu	Arg	Ala							
		110									

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GAGTGTTGTA CAGCCTCC

18

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

TGCCCCGAAA TTTGGGC

17

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid

T09070-20F66860

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

TGCCCCGAGA TTTGGG

16

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

GAGTGTGGAA CAGCCTC

17

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

GGGGGCCTGG AGGCTG

16

0969302.070501